

In the Claims

Please amend the claims as follows.

1. (Original) An isolated polypeptide having the ability to bind to KDR or VEGF/KDR complex comprising an amino acid sequence of one of the following:

Loop Consensus Sequence 15: Cys-X₂-X₃-X₄-X₅-X₆-X₇-Cys (TN8), wherein

X₂ is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X₃ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₄ is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X₅ is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X₆ is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X₇ is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16: Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-Cys (TN12), wherein

X₂ is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X₃ is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X₄ is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X₅ is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X₆ is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X₇ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₈ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X₉ is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₁₀ is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X₁₁ is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X₂-X₃-X₄-Gly-X₆-Cys (TN7), wherein

X₂ is Asn, Asp or Glu;

X₃ is Glu, His, Lys or Phe;

X₄ is Asp, Gln, Leu, Lys, Met or Tyr; and

X₆ is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-Cys (TN9), wherein

X₂ is Ala, Asp, Lys, Ser, Trp or Val;

X₃ is Asn, Glu, Gly, His or Leu;

X₄ is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X₅ is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X₆ is His, Pro or Trp;

X₇ is Ala, Gly, His, Leu, Trp or Tyr; and

X₈ is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X₂-X₃-X₄-X₅-Ser-Gly-Pro-X₉-X₁₀-X₁₁-X₁₂-Cys (MTN13; SEQ ID NO:1), wherein

X₂ is Asp, Glu, His or Thr;

X₃ is Arg, His, Lys or Phe;

X₄ is Gln, Ile, Lys, Tyr or Val;

X₅ is Gln, Ile, Leu, Met or Phe;

X₉ is Asn, Asp, Gly, His or Tyr;

X₁₀ is Gln, Gly, Ser or Thr;

X₁₁ is Glu, Lys, Phe or Ser; and

X₁₂ is Glu, Ile, Ser or Val.

2. (Original) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of one of the following:

Loop Consensus Sequence 20: Cys-X₂-X₃-X₄-X₅-X₆-Tyr-Cys (TN8), wherein

X₂ is Ala, Arg, Glu, Lys or Ser;

X₃ is Ala, Asp, Gln, Glu, Thr or Val;

X₄ is Asp or Glu;

X₅ is Trp or Tyr; and

X₆ is Thr or Tyr; or

Loop Consensus Sequence 21: Cys-X₂-X₃-X₄-Gly-X₆-X₇-Cys (TN8), wherein

X₂ is Asp, Gln or His;

X₃ is His or Tyr;

X₄ is His, Ile or Tyr;

X₆ is Ile, Met or Val; and

X₇ is Gly or Tyr; or

Loop Consensus Sequence 22: Cys-X₂-X₃-X₄-X₅-Gly-X₇-Cys (TN8), wherein

X₂ is Ala, Arg, Asn, Asp, His, Phe, Trp or Tyr;

X₃ is Ala, Asp, Gln, His, Lys, Met, Ser, Thr, Trp, Tyr or Val;

X₄ is Ala, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr or Val;

X₅ is Asp, Phe, Ser, Thr, Trp or Tyr; and

X₇ is Ala, Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr.

3. (Original) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of one of the following:

Loop Consensus Sequence 23: Cys-X₂-X₃-X₄-X₅-Trp-Gly-Gly-X₉-X₁₀-Cys (SEQ ID NO:3; TN11), wherein

X₂ is Ala, Phe or Trp;

X₃ is Glu or Lys;

X₄ is Asp, Ser, Trp or Tyr;

X₅ is Phe, Pro or Ser;

X₉ is Gln or Glu; and

X₁₀ is Ile, Phe or Val; or

Loop Consensus Sequence 24: Cys-X₂-Glu-X₄-Ser-X₆-Ser-X₈-X₉-X₁₀-Phe-Cys (SEQ ID NO:15; TN12), wherein

X₂ is His or Tyr;

X₄ is Leu, His or Thr;

X₆ is Asp or Leu;

X₈ is Gly or Val;

X₉ is Thr or Val; and

X₁₀ is Arg or Trp; or

Loop Consensus Sequence 25: Cys-X₂-X₃-X₄-X₅-X₆-X₇-Gly-X₉-Trp-X₁₁-Cys (TN12; SEQ ID NO:16), wherein

X₂ is Glu, Met or Thr;

X₃ is Ile, Leu, Met or Phe;

X₄ is Arg, Asp, Glu, Met, Trp or Val;

X₅ is Asn, Gln, Gly, Ser or Val;

X₆ is Glu or Asp;

X₇ is Lys, Ser, Thr or Val;

X₉ is Arg, Gln, Lys or Trp; and

X₁₁ is Asn, Leu, Phe or Tyr; or

Loop Consensus Sequence 26: Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-Cys (TN12), wherein

X₂ is Glu or Gly;

X₃ is Trp or Tyr;

X₄ is Ser or Thr;

X₅ is Asn or Gln;

X₆ is Gly or Met;

X₇ is Phe or Tyr;

X₈ is Asp or Gln;

X₉ is Lys or Tyr;

X₁₀ is Glu or Thr; and

X₁₁ is Glu or Phe.

4. (Original) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 27: Cys-X₂-X₃-X₄-Gly-X₆-Cys (TN7), wherein

X₂ is Asn, Asp or Glu;

X₃ is Glu, His, Lys or Phe;

X₄ is Asp, Gln, Leu, Lys, Met or Tyr; and

X₆ is Arg, Gln, Leu, Lys or Val.

5. (Original) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 28: Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-Cys (TN9), wherein

X₂ is Ala, Lys, Ser, Trp or Val;

X₃ is Asn, Glu, Gly, His or Leu;

X₄ is Glu, Gly, Lys, Met or Tyr;

X₅ is Ala, Asn, Asp, Leu, Met, Pro or Ser;

X₆ is His, Pro or Trp;

X₇ is His, Leu, Trp or Tyr; and

X₈ is Ala, Asp, Gln, Leu, Met, Thr or Trp.

6. (Original) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 29: Cys-X₂-X₃-X₄-X₅-Ser-Gly-Pro-X₉-X₁₀-X₁₁-X₁₂-Cys (SEQ ID NO:1; MTN13), wherein

X₂ is Asp, Glu, His or Thr;

X₃ is Arg, His, Lys or Phe;

X₄ is Gln, Ile, Lys, Tyr or Val;

X₅ is Gln, Ile, Leu, Met or Phe;

X₉ is Asn, Asp, Gly, His or Tyr;

X₁₀ is Gln, Gly, Ser or Thr;

X₁₁ is Glu, Lys, Phe or Ser; and

X₁₂ is Glu, Ile, Ser or Val.

7. (Original) An isolated polypeptide having the ability to bind to KDR or VEGF/KDR complex comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-Cys-X₁₂-X₁₃-X₁₄ (TN8), wherein

X₁ is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X₂ is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X₃ is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X₅ is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X₆ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₇ is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₈ is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X₉ is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X₁₀ is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X₁₂ is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₁₃ is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X₁₄ is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-X₁₂-X₁₃-X₁₄-Cys-X₁₆-X₁₇-X₁₈ (TN12), wherein

X₁ is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X₂ is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X₃ is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₅ is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X₆ is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X₇ is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X₈ is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X₉ is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X₁₀ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₁₁ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X₁₂ is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₁₃ is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X₁₄ is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X₁₆ is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₁₇ is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X₁₈ is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X₁-X₂-X₃-Cys-X₅-X₆-X₇-Gly-X₉-Cys-X₁₁-X₁₂-X₁₃ (TN7),
wherein

X₁ is Gly or Trp;

X₂ is Ile, Tyr or Val;

X₃ is Gln, Glu, Thr or Trp;

X₅ is Asn, Asp or Glu;

X₆ is Glu, His, Lys or Phe;

X₇ is Asp, Gln, Leu, Lys, Met or Tyr;

X₉ is Arg, Gln, Leu, Lys or Val;

X₁₁ is Arg, Phe, Ser, Trp or Val;

X₁₂ is Glu, His or Ser; and

X₁₃ is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-Cys-X₁₃-X₁₄-X₁₅ (TN9),
wherein

X₁ is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X₂ is Asp, Gly, His, Pro or Trp;

X₃ is Gly, Pro, Phe, Thr or Trp;

X₅ is Ala, Asp, Lys, Ser, Trp or Val;

X₆ is Asn, Glu, Gly, His or Leu;

X₇ is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X₈ is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X₉ is His, Pro or Trp;

X₁₀ is Ala, Gly, His, Leu, Trp or Tyr;

X₁₁ is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X₁₃ is Ala, Lys, Ser, Trp or Tyr;

X₁₄ is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X₁₅ is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-Ser-Gly-Pro-X₁₂-X₁₃-X₁₄-X₁₅-Cys-X₁₇-X₁₈-X₁₉ (SEQ ID NO:1; MTN13), wherein

X₁ is Arg, Glu, His, Ser or Trp;

X₂ is Asn, Asp, Leu, Phe, Thr or Val;

X₃ is Arg, Asp, Glu, His, Lys or Thr;

X₅ is Asp, Glu, His or Thr;

X₆ is Arg, His, Lys or Phe;

X₇ is Gln, Ile, Lys, Tyr or Val;

X₈ is Gln, Ile, Leu, Met or Phe;

X₁₂ is Asn, Asp, Gly, His or Tyr;

X₁₃ is Gln, Gly, Ser or Thr;

X₁₄ is Glu, Lys, Phe or Ser;

X₁₅ is Glu, Ile, Ser or Val;

X₁₇ is Glu, Gly, Lys, Phe, Ser or Val;

X₁₈ is Arg, Asn, Ser or Tyr; and

X₁₉ is Asp, Gln, Glu, Gly, Met or Tyr.

8. (Original) The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 6: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-Tyr-Cys-X₁₂-X₁₃-X₁₄, wherein

X₁ is Ala, Arg, Asp, Leu, Lys, Pro, Ser or Val;

X₂ is Asn, Asp, Glu, Lys, Thr or Ser;

X₃ is Ile, Leu, Trp;

X₅ is Ala, Arg, Glu, Lys or Ser;

X₆ is Ala, Asp, Gln, Glu, Thr or Val;

X₇ is Asp or Glu;

X₈ is Trp or Tyr;

X₉ is Thr or Tyr;

X₁₂ is Glu, Met, Phe, Trp or Tyr;

X₁₃ is Ile, Leu or Met; and

X₁₄ is Ile, Leu, Met, Phe or Thr; or

Consensus Sequence 7: Trp-Tyr-Trp-Cys-X₅-X₆-X₇-Gly-X₉-X₁₀-Cys-X₁₂-X₁₃-X₁₄ (SEQ ID NO:2), wherein

X₅ is Asp, Gln or His;

X₆ is His or Tyr;

X₇ is Ile, His or Tyr;

X₉ is Ile, Met or Val;

X₁₀ is Gly or Tyr;

X₁₂ is Asp, Lys or Pro;

X₁₃ is Gln, Gly or Trp; and

X₁₄ is Phe, Ser or Thr; or

Consensus Sequence 8: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-Gly-X₁₀-Cys-X₁₂-X₁₃-X₁₄, wherein

X₁ is Gly, Leu, His, Thr, Trp, Tyr;

X₂ is Ile, Leu, Thr, Trp or Val;

X₃ is Asp, Glu, Gln, Trp or Thr;

X₅ is Ala, Arg, Asn, Asp, His, Phe, Trp or Tyr;

X₆ is Ala, Asp, Gln, His, Lys, Met, Ser, Thr, Trp, Tyr or Val;

X₇ is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr or Val;

X₈ is Asp, Phe, Ser, Thr, Trp or Tyr;

X₁₀ is Ala, Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X₁₂ is Arg, Gln, His, Ile, Lys, Met, Phe, Thr, Trp, Tyr or Val;

X₁₃ is Arg, Asn, Asp, Glu, His, Met, Pro, Ser or Thr; and

X₁₄ is Arg, Gln, Glu, Gly, Phe, Ser, Trp or Tyr.

9. (Original) The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 9: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-Trp-Gly-Gly-X₁₂-X₁₃-Cys-X₁₅-X₁₆-X₁₇ (SEQ ID NO:3), wherein

X₁ is Ser, Phe, Trp, Tyr or Gly;

X₂ is Arg, Gly, Ser or Trp;

X₃ is Ala, Glu, Ile or Val;

X₅ is Ala, Phe or Trp;

X₆ is Glu or Lys;

X₇ is Asp, Ser or Trp;

X₈ is Phe, Pro or Ser;

X₁₂ is Gln or Glu;

X₁₃ is Ile, Phe or Val;

X₁₅ is Gln, Ile, Leu or Phe;

X₁₆ is Arg, Gly or Pro; and

X₁₇ is Gln, His, Phe, Ser, Tyr or Val; or

Consensus Sequence 10: Tyr-Pro-X₃-Cys-X₅-Glu-X₇-Ser-X₉-Ser-X₁₁-X₁₂-X₁₃-Phe-Cys-X₁₆-X₁₇-X₁₈ (SEQ ID NO:4; TN12), wherein

X₃ is Gly or Trp;

X₅ is His or Tyr;

X₇ is His, Leu or Thr;

X₉ is Asp or Leu;

X₁₁ is Gly or Val;

X₁₂ is Thr or Val;

X₁₃ is Arg or Trp;

X₁₆ is Ala or Val;

X₁₇ is Asp or Pro; and

X₁₈ is Gly or Trp; or

Consensus Sequence 11: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-Gly-X₁₂-Trp-X₁₄-Cys-X₁₆-X₁₇-X₁₈ (SEQ ID NO:5; TN12), wherein

X₁ is Asp, Gly, Pro or Ser;

X₂ is Arg, Asn, Asp, Gly or Ser;

X₃ is Gly, Thr, Trp or Tyr;

X₅ is Glu, Met or Thr;

X₆ is Ile, Leu, Met or Phe;

X₇ is Arg, Asp, Glu, Met, Trp or Val;

X₈ is Asn, Gln, Gly, Ser or Val;

X₉ is Asp or Glu;

X₁₀ is Lys, Ser, Thr or Val;

X₁₂ is Arg, Gln, Lys or Trp;

X₁₄ is Asn, Leu, Phe or Tyr;

X₁₆ is Gly, Phe, Ser or Tyr;

X₁₇ is Gly, Leu, Pro or Ser; and

X₁₈ is Ala, Asp, Pro, Ser, Trp or Tyr; or

Consensus Sequence 12: Asn-Trp-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-X₁₂-X₁₃-X₁₄-Cys-X₁₆-X₁₇-X₁₈ (SEQ ID NO:6; TN12), wherein

X₃ is Glu or Lys;

X₅ is Glu or Gly;

X₆ is Trp or Tyr;

X₇ is Ser or Thr;

X₈ is Asn or Gln;
X₉ is Gly or Met;
X₁₀ is Phe or Tyr;
X₁₁ is Asp or Gln;
X₁₂ is Lys or Tyr;
X₁₃ is Glu or Thr;
X₁₄ is Glu or Phe;
X₁₆ is Ala or Val;
X₁₇ is Arg or Tyr; and
X₁₈ is Leu or Pro,

wherein the polypeptide binds KDR or a VEGF/KDR complex.

10. (Original) An isolated polypeptide having the ability to bind to KDR or VEGF/KDR complex comprising an amino acid sequence of one of the following:

Consensus Sequence 13: Z₁-X₁-X₂-X₃-X₄-X₅-Z₂ (Lin20); wherein,

Z₁ is a polypeptide of at least one amino acid or is absent;
X₁ is Ala, Asp, Gln or Glu;
X₂ is Ala, Asp, Gln, Glu, Pro;
X₃ is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;
X₄ is Asp, Leu, Ser, Trp, Tyr or Val;
X₅ is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and
Z₂ is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X₁-X₂-X₃-Tyr-Trp-Glu-X₇-X₈-X₉-Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X₁ is Asp, Gly or Ser;
X₂ is Ile, Phe or Tyr;
X₃ is Ala, Ser or Val;
X₇ is Gln, Glu, Ile or Val;

X₈ is Ala, Ile or Val;

X₉ is Ala, Glu, Val or Thr; and

11. (Original) The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 20-86, 87-136, 187-192, 193-203, and 207-259.
12. (Original) The polypeptide of Claim 10, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 137-186.
13. (Original) The polypeptide of one of Claims 1, 7 or 10, wherein the polypeptide further comprises N-terminal and/or C-terminal flanking peptides of one or more amino acids.
14. (Original) The polypeptide of one of Claims 1, 7 or 10, wherein the polypeptide comprises a modification selected from the group consisting of: an amino acid substitution, and amide bond substitution, a D-amino acid substitution, a glycosylated amino acid, a disulfide bond, a disulfide mimetic substitution, an amino acid translocation, a retroinverso peptide, a peptoid, a retro-inverso peptoid, and a synthetic peptide.
15. (Original) The polypeptide of one of Claims 1, 7 or 10, wherein the polypeptide is conjugated to one or more detectable labels or therapeutic agents, optionally further comprising a linker or spacer between the polypeptide and the detectable label or the therapeutic agent.
16. (Original) The polypeptide of Claim 15, wherein the detectable label or the therapeutic agent is selected from the group consisting of: an enzyme, a fluorescent compound, a liposome, an optical dye, one or more paramagnetic metal ions or a superparamagnetic particle, an ultrasound contrast agent and one or more radionuclides.

17. (Original) The polypeptide of Claim 16, wherein the therapeutic agent or detectable label comprises one or more radionuclides.
18. (Original) The polypeptide of Claim 17, wherein the radionuclide is selected from the group consisting of: ^{18}F , ^{124}I , ^{125}I , ^{131}I , ^{123}I , ^{77}Br , ^{76}Br , $^{99\text{m}}\text{Tc}$, ^{51}Cr , ^{67}Ga , ^{68}Ga , ^{47}Sc , ^{51}Cr , ^{167}Tm , ^{141}Ce , ^{111}In , ^{168}Yb , ^{175}Yb , ^{140}La , ^{90}Y , ^{88}Y , ^{153}Sm , ^{166}Ho , ^{165}Dy , ^{166}Dy , ^{62}Cu , ^{64}Cu , ^{67}Cu , ^{97}Ru , ^{103}Ru , ^{186}Re , ^{188}Re , ^{203}Pb , ^{211}Bi , ^{212}Bi , ^{213}Bi , ^{214}Bi , ^{105}Rh , ^{109}Pd , $^{117\text{m}}\text{Sn}$, ^{149}Pm , ^{161}Tb , ^{177}Lu , ^{198}Au and ^{199}Au .
19. (Original) The polypeptide of Claim 18, wherein the therapeutic agent or detectable label further comprises a chelator.
20. (Original) The polypeptide of Claim 19, wherein the chelator comprises a compound selected from the group consisting of: formula 20, 21, 22, 23a, 23b, 24a, 24b, and 25.
21. (Original) The polypeptide of Claim 19, wherein the radionuclide is $^{99\text{m}}\text{Tc}$ or ^{111}In .
22. (Original) The polypeptide of Claim 19, wherein the radionuclide is selected from the group consisting of: ^{177}Lu , ^{90}Y , ^{153}Sm and ^{166}Ho .
23. (Original) The polypeptide of Claim 16, wherein the detectable label comprises an ultrasound contrast agent.
24. (Original) The polypeptide of Claim 23, wherein the ultrasound contrast agent is a phospholipid stabilized microbubble or an ultrasound contrast agent comprising a gas.
25. (Original) The polypeptide of Claim 24, wherein the ultrasound contrast agent comprises a fluorinated gas.

26. (Original) The polypeptide of Claim 16, wherein the detectable label comprises one or more paramagnetic metal ions and one or more chelators.
27. (Original) The polypeptide of Claim 15, wherein the therapeutic agent is selected from the group consisting of: a bioactive agent, a cytotoxic agent, a drug, a chemotherapeutic agent and a radiotherapeutic agent.
- 28-31 (Canceled)
32. (Original) A method for isolating phage that bind KDR or a VEGF/KDR complex, comprising the steps of:
- (a) immobilizing a KDR or VEGF/KDR complex target on a solid support;
 - (b) contacting a library of potential KDR or VEGF/KDR complex binding phage with the solid support to bind KDR or a VEGF/KDR complex binding phage in the library; and
 - (c) removing the unbound portion of the phage library from the solid support, thereby isolating phage that bind KDR or a VEGF/KDR complex.
- 33-52. (Canceled)
53. (Original) A recombinant bacteriophage displaying a KDR binding or VEGF/KDR complex binding polypeptide, which polypeptide comprises an amino acid sequence of one of the following:
- Consensus Sequence 1: $X_1-X_2-X_3$ -Cys- $X_5-X_6-X_7-X_8-X_9-X_{10}$ -Cys- $X_{12}-X_{13}-X_{14}$ (TN8), wherein
- X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;
 - X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;
 - X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;
 - X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X₆ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₇ is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₈ is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X₉ is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X₁₀ is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X₁₂ is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₁₃ is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X₁₄ is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-X₁₂-X₁₃-X₁₄-Cys-X₁₆-X₁₇-X₁₈ (TN12), wherein

X₁ is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X₂ is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X₃ is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₅ is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X₆ is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X₇ is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X₈ is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X₉ is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X₁₀ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₁₁ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X₁₂ is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₁₃ is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X₁₄ is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X₁₆ is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₁₇ is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X₁₈ is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X₁-X₂-X₃-Cys-X₅-X₆-X₇-Gly-X₉-Cys-X₁₁-X₁₂-X₁₃ (TN7),

wherein

X₁ is Gly or Trp;

X₂ is Ile, Tyr or Val;

X₃ is Gln, Glu, Thr or Trp;

X₅ is Asn, Asp or Glu;

X₆ is Glu, His, Lys or Phe;

X₇ is Asp, Gln, Leu, Lys, Met or Tyr;

X₉ is Arg, Gln, Leu, Lys or Val;

X₁₁ is Arg, Phe, Ser, Trp or Val;

X₁₂ is Glu, His or Ser; and

X₁₃ is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-Cys-X₁₃-X₁₄-X₁₅ (TN9),

wherein

X₁ is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X₂ is Asp, Gly, His, Pro or Trp;

X₃ is Gly, Pro, Phe, Thr or Trp;

X₅ is Ala, Asp, Lys, Ser, Trp or Val;

X₆ is Asn, Glu, Gly, His or Leu;

X₇ is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X₈ is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X₉ is His, Pro or Trp;

X₁₀ is Ala, Gly, His, Leu, Trp or Tyr;

X₁₁ is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X₁₃ is Ala, Lys, Ser, Trp or Tyr;

X₁₄ is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X₁₅ is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-Ser-Gly-Pro-X₁₂-X₁₃-X₁₄-X₁₅-Cys-X₁₇-X₁₈-X₁₉ (SEQ ID NO:1; MTN13), wherein

X₁ is Arg, Glu, His, Ser or Trp;

X₂ is Asn, Asp, Leu, Phe, Thr or Val;

X₃ is Arg, Asp, Glu, His, Lys or Thr;

X₅ is Asp, Glu, His or Thr;

X₆ is Arg, His, Lys or Phe;

X₇ is Gln, Ile, Lys, Tyr or Val;

X₈ is Gln, Ile, Leu, Met or Phe;

X₁₂ is Asn, Asp, Gly, His or Tyr;

X₁₃ is Gln, Gly, Ser or Thr;

X₁₄ is Glu, Lys, Phe or Ser;

X₁₅ is Glu, Ile, Ser or Val;

X₁₇ is Glu, Gly, Lys, Phe, Ser or Val;

X₁₈ is Arg, Asn, Ser or Tyr; and

X₁₉ is Asp, Gln, Glu, Gly, Met or Tyr,

and wherein the polypeptide is displayed on the surface of the recombinant bacteriophage.

54. (Original) A magnetic resonance imaging contrast agent comprising a KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-Cys-X₁₂-X₁₃-X₁₄ (TN8), wherein

X₁ is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X₂ is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X₃ is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X₅ is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X₆ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₇ is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₈ is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X₉ is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X₁₀ is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X₁₂ is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₁₃ is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X₁₄ is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-X₁₂-X₁₃-X₁₄-Cys-X₁₆-X₁₇-X₁₈ (TN12), wherein

X₁ is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X₂ is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X₃ is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₅ is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X₆ is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X₇ is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X₈ is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X₉ is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X₁₀ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₁₁ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X₁₂ is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₁₃ is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X₁₄ is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X₁₆ is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₁₇ is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X₁₈ is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X₁-X₂-X₃-Cys-X₅-X₆-X₇-Gly-X₉-Cys-X₁₁-X₁₂-X₁₃ (TN7),
wherein

X₁ is Gly or Trp;
X₂ is Ile, Tyr or Val;
X₃ is Gln, Glu, Thr or Trp;
X₅ is Asn, Asp or Glu;
X₆ is Glu, His, Lys or Phe;
X₇ is Asp, Gln, Leu, Lys, Met or Tyr;
X₉ is Arg, Gln, Leu, Lys or Val;
X₁₁ is Arg, Phe, Ser, Trp or Val;
X₁₂ is Glu, His or Ser; and
X₁₃ is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-Cys-X₁₃-X₁₄-X₁₅ (TN9),
wherein

X₁ is Arg, Asp, Gly, Ile, Met, Pro or Tyr;
X₂ is Asp, Gly, His, Pro or Trp;
X₃ is Gly, Pro, Phe, Thr or Trp;
X₅ is Ala, Asp, Lys, Ser, Trp or Val;
X₆ is Asn, Glu, Gly, His or Leu;
X₇ is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;
X₈ is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;
X₉ is His, Pro or Trp;
X₁₀ is Ala, Gly, His, Leu, Trp or Tyr;
X₁₁ is Ala, Asp, Gln, Leu, Met, Thr or Trp;
X₁₃ is Ala, Lys, Ser, Trp or Tyr;
X₁₄ is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and
X₁₅ is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-Ser-Gly-Pro-X₁₂-X₁₃-X₁₄-X₁₅-Cys-X₁₇-X₁₈-X₁₉ (SEQ ID NO:1; MTN13), wherein

X₁ is Arg, Glu, His, Ser or Trp;

X₂ is Asn, Asp, Leu, Phe, Thr or Val;

X₃ is Arg, Asp, Glu, His, Lys or Thr;

X₅ is Asp, Glu, His or Thr;

X₆ is Arg, His, Lys or Phe;

X₇ is Gln, Ile, Lys, Tyr or Val;

X₈ is Gln, Ile, Leu, Met or Phe;

X₁₂ is Asn, Asp, Gly, His or Tyr;

X₁₃ is Gln, Gly, Ser or Thr;

X₁₄ is Glu, Lys, Phe or Ser;

X₁₅ is Glu, Ile, Ser or Val;

X₁₇ is Glu, Gly, Lys, Phe, Ser or Val;

X₁₈ is Arg, Asn, Ser or Tyr; and

X₁₉ is Asp, Gln, Glu, Gly, Met or Tyr,

wherein the polypeptide is coupled to at least one chelator capable of complexing a paramagnetic metal or at least one superparamagnetic particle, and wherein the polypeptide optionally comprises an N-terminal and/or C-terminal flanking peptide.

55-75. (Canceled)

76. (Original) A multimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR complex comprising at least one amino acid selected from the group consisting of:

Loop Consensus Sequence 15: Cys-X₂-X₃-X₄-X₅-X₆-X₇-Cys (TN8), wherein

X₂ is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X₃ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₄ is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₅ is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X₆ is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or
Loop Consensus Sequence 16: Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-Cys (TN12), wherein

X₂ is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;
X₃ is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;
X₄ is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;
X₅ is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;
X₆ is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;
X₇ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;
X₈ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;
X₉ is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;
X₁₀ is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and
X₁₁ is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X₂-X₃-X₄-Gly-X₆-Cys (TN7), wherein

X₂ is Asn, Asp or Glu;
X₃ is Glu, His, Lys or Phe;
X₄ is Asp, Gln, Leu, Lys, Met or Tyr; and
X₆ is Arg, Gln, Leu, Lys or Val; or
Consensus Sequence IV: Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-Cys (TN9), wherein
X₂ is Ala, Asp, Lys, Ser, Trp or Val;
X₃ is Asn, Glu, Gly, His or Leu;
X₄ is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;
X₅ is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;
X₆ is His, Pro or Trp;
X₇ is Ala, Gly, His, Leu, Trp or Tyr; and
X₈ is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 18: Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-Cys (TN9), wherein

X₂ is Ala, Asp, Lys, Ser, Trp or Val;
X₃ is Asn, Glu, Gly, His or Leu;

X₄ is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X₅ is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X₆ is His, Pro or Trp;

X₇ is Ala, Gly, His, Leu, Trp or Tyr; and

X₈ is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X₂-X₃-X₄-X₅-Ser-Gly-Pro-X₉-X₁₀-X₁₁-X₁₂-Cys (MTN13; SEQ ID NO:1), wherein

X₂ is Asp, Glu, His or Thr;

X₃ is Arg, His, Lys or Phe;

X₄ is Gln, Ile, Lys, Tyr or Val;

X₅ is Gln, Ile, Leu, Met or Phe;

X₉ is Asn, Asp, Gly, His or Tyr;

X₁₀ is Gln, Gly, Ser or Thr;

X₁₁ is Glu, Lys, Phe or Ser; and

X₁₂ is Glu, Ile, Ser or Val.

77. (Canceled)

78. (Original) A multimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR complex comprising at least one amino acid sequence of one of the following:

Consensus Sequence 13: Z₁-X₁-X₂-X₃-X₄-X₅-Z₂ (Lin20); wherein,

Z₁ is a polypeptide of at least one amino acid or is absent;

X₁ is Ala, Asp, Gln or Glu;

X₂ is Ala, Asp, Gln, Glu, Pro;

X₃ is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X₄ is Asp, Leu, Ser, Trp, Tyr or Val;

X₅ is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z₂ is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X₁-X₂-X₃-Tyr-Trp-Glu-X₇-X₈-X₉-Leu (Lin20; SEQ ID

NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X₁ is Asp, Gly or Ser;

X₂ is Ile, Phe or Tyr;

X₃ is Ala, Ser or Val;

X₇ is Gln, Glu, Ile or Val;

X₈ is Ala, Ile or Val;

X₉ is Ala, Glu, Val or Thr.

79-157. (Canceled)

158. (Currently Amended) A method of detecting KDR or VEGF/KDR complex in an animal or human subject and optionally imaging at least a portion of the animal or human subject comprising the steps of:

- (a) detectably labeling a multimeric polypeptide construct of one of Claims 76, ~~77~~ or 78;
- (b) administering to the subject the labeled multimeric polypeptide construct; and,
- (c) detecting the labeled multimeric polypeptide construct in the subject, and, optionally, constructing an image..

159-174. (Canceled)

175. (Original) A multimeric polypeptide having the ability to bind to KDR or VEGF/KDR complex selected from the group consisting of: D30 and D31.

176-194. (Canceled)

195. (Original) A method of inhibiting VEGF activation of KDR comprising administering to

an animal or human subject in need of treatment for such condition a polypeptide having the ability to bind to KDR or VEGF/KDR complex, or a multimeric polypeptide construct comprising at least one polypeptide having the ability to bind to KDR or VEGF/KDR complex, said polypeptide comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X_1 - X_2 - X_3 -Cys- X_5 - X_6 - X_7 - X_8 - X_9 - X_{10} -Cys- X_{12} - X_{13} - X_{14}

(TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1 - X_2 - X_3 -Cys- X_5 - X_6 - X_7 - X_8 - X_9 - X_{10} - X_{11} - X_{12} - X_{13} - X_{14} -Cys- X_{16} - X_{17} - X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X₇ is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;
X₈ is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;
X₉ is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;
X₁₀ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;
X₁₁ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;
X₁₂ is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;
X₁₃ is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;
X₁₄ is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;
X₁₆ is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;
X₁₇ is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and
X₁₈ is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X₁-X₂-X₃-Cys-X₅-X₆-X₇-Gly-X₉-Cys-X₁₁-X₁₂-X₁₃ (TN7),

wherein

X₁ is Gly or Trp;
X₂ is Ile, Tyr or Val;
X₃ is Gln, Glu, Thr or Trp;
X₅ is Asn, Asp or Glu;
X₆ is Glu, His, Lys or Phe;
X₇ is Asp, Gln, Leu, Lys, Met or Tyr;
X₉ is Arg, Gln, Leu, Lys or Val;
X₁₁ is Arg, Phe, Ser, Trp or Val;
X₁₂ is Glu, His or Ser; and
X₁₃ is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-Cys-X₁₃-X₁₄-X₁₅ (TN9),

wherein

X₁ is Arg, Asp, Gly, Ile, Met, Pro or Tyr;
X₂ is Asp, Gly, His, Pro or Trp;
X₃ is Gly, Pro, Phe, Thr or Trp;
X₅ is Ala, Asp, Lys, Ser, Trp or Val;

X₆ is Asn, Glu, Gly, His or Leu;

X₇ is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X₈ is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X₉ is His, Pro or Trp;

X₁₀ is Ala, Gly, His, Leu, Trp or Tyr;

X₁₁ is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X₁₃ is Ala, Lys, Ser, Trp or Tyr;

X₁₄ is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X₁₅ is Asn, Gln, Glu, Leu, Met, Pro or Trp;

Consensus Sequence 5: X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-Ser-Gly-Pro-X₁₂-X₁₃-X₁₄-X₁₅-Cys-X₁₇-X₁₈-X₁₉ (SEQ ID NO:1; MTN13), wherein

X₁ is Arg, Glu, His, Ser or Trp;

X₂ is Asn, Asp, Leu, Phe, Thr or Val;

X₃ is Arg, Asp, Glu, His, Lys or Thr;

X₅ is Asp, Glu, His or Thr;

X₆ is Arg, His, Lys or Phe;

X₇ is Gln, Ile, Lys, Tyr or Val;

X₈ is Gln, Ile, Leu, Met or Phe;

X₁₂ is Asn, Asp, Gly, His or Tyr;

X₁₃ is Gln, Gly, Ser or Thr;

X₁₄ is Glu, Lys, Phe or Ser;

X₁₅ is Glu, Ile, Ser or Val;

X₁₇ is Glu, Gly, Lys, Phe, Ser or Val;

X₁₈ is Arg, Asn, Ser or Tyr; and

X₁₉ is Asp, Gln, Glu, Gly, Met or Tyr;

Consensus Sequence 13: Z₁-X₁-X₂-X₃-X₄-X₅-Z₂ (Lin20); wherein,

Z₁ is a polypeptide of at least one amino acid or is absent;

X₁ is Ala, Asp, Gln or Glu;

X₂ is Ala, Asp, Gln, Glu, Pro;

X₃ is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X₄ is Asp, Leu, Ser, Trp, Tyr or Val;

X₅ is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z₂ is a polypeptide of at least one amino acid or is absent;

Consensus Sequence 14: X₁-X₂-X₃-Tyr-Trp-Glu-X₇-X₈-X₉-Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X₁ is Asp, Gly or Ser;

X₂ is Ile, Phe or Tyr;

X₃ is Ala, Ser or Val;

X₇ is Gln, Glu, Ile or Val;

X₈ is Ala, Ile or Val;

X₉ is Ala, Glu, Val or Thr;

Loop Consensus Sequence 15: Cys-X₂-X₃-X₄-X₅-X₆-X₇-Cys (TN8), wherein

X₂ is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X₃ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₄ is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X₅ is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X₆ is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X₇ is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16: Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-Cys (TN12), wherein

X₂ is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X₃ is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X₄ is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X₅ is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X₆ is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X₇ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X₈ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X₉ is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X₁₀ is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X₁₁ is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X₂-X₃-X₄-Gly-X₆-Cys (TN7), wherein

X₂ is Asn, Asp or Glu;

X₃ is Glu, His, Lys or Phe;

X₄ is Asp, Gln, Leu, Lys, Met or Tyr; and

X₆ is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-Cys (TN9), wherein

X₂ is Ala, Asp, Lys, Ser, Trp or Val;

X₃ is Asn, Glu, Gly, His or Leu;

X₄ is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X₅ is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X₆ is His, Pro or Trp;

X₇ is Ala, Gly, His, Leu, Trp or Tyr; and

X₈ is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X₂-X₃-X₄-X₅-Ser-Gly-Pro-X₉-X₁₀-X₁₁-X₁₂-Cys (MTN13; SEQ ID NO:1), wherein

X₂ is Asp, Glu, His or Thr;

X₃ is Arg, His, Lys or Phe;

X₄ is Gln, Ile, Lys, Tyr or Val;

X₅ is Gln, Ile, Leu, Met or Phe;

X₉ is Asn, Asp, Gly, His or Tyr;

X₁₀ is Gln, Gly, Ser or Thr;

X₁₁ is Glu, Lys, Phe or Ser; and

X₁₂ is Glu, Ile, Ser or Val.

196-197. (Canceled)